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E CTG	H CX	ء دی دی	c c:	ا تح ،	I ATC	cuc A	r cre	R AGG	L CTC	R CCCG	H CAC	r. CTC	N AAC	I ATC	n aat	λ ccc	I	R CCCC	D GAC	Y TAC	227 311
.cc	F	K C AA	G A	R X	r CLC	Y TAC	R CGA	L CTC	K AAG	orc v	L	E GAG	I ATC	s TCC	H CAC	100 W	CCC P	Y TAC	L TR	D GAC	247
T ACC	H Th	. T	<b>3</b> 0	P CC	N AAC	с 100	r cro	Y TAC	G GGC	r Cuc	N AAC	L CTG	T ACG	S	r CIG	S TCC	I ATC	Τ : λ <b>ω</b>	H CW	. 1000	26 <b>7</b> 931
N	r CT	I	e e	A CT	org Gra	P P	Y TAC	L CTG	A GCC	v Gre	s R	H CAC	L CIA	v Gre	Y TAT	r CIC	R	F TTC	r C	N AAC	2 <b>87</b> 9 <b>91</b>
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Q	5 G2	i i	rc c	Q Q	r CIC	v GTC	G GGC	G : CCC	Q	L CTC	A GCC	v : crc	v Green	E GAC	. ccc	Y TAT	GCC A	F TTC	R CO	G G GGG	327
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Docket/Appl'n No.: 10/718,332

Title: Novel Genes Encoding Proteins ...

Inventors: Sean A. McCarthy, et al. Replacement Sheet

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FIG. 1B

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Percent	Similarity: 49.308 Percent Identity: 29.412
T79	1 MLAGGVRSMPSPLLACWQPILLLVLGSVLSGSATGCPPRCECSAQDR. 47 :         :
D4591	48AVLCHRKRFVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS 87
D459:	:   : : : : : :     -   -   -   -
<b>T</b> 79	88 FPHLEELELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLS 137
D459	3 85AKTVDELQQLFNLTELDFSQNNFTNIKEVGLANLT 119
T79	138 NLTKLDTRENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNSL 187
D459	13 120 QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNQISTISANAFSGLKNL 189
T79	
D459	13 170 LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVIGILDMNFRPLSNLRS 219  238 LEISHWPYLDTMTPNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL 286
	:.   :. :     :  .   : :
179	287 NLSYNPISTIEGSMLHELLRLQEIQLVG.GQLAVVEPY
D45	13 269 DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKLE 318
т79	324AFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLIL 360
D45	
T79	.        :  ::       .:    :  :
D45	
T79	110 PNYFT.CRRARTRDRRAQQVFVDEGRTVQTVCREEDEDTVCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	450 LYSAKS NGBLTUFPDGTLFVRYAOVODNGTYLCIAANAGGNDSMPAHLH 507
	:::::::::::::::::::::::::::::::::::
•	508 VRSYSPDWPHQ 518
D4:	913 516 VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN 565
т7	519 PNKTFAFISNQPGEGEANSTRA 540

045913	5 <b>66</b>	:  : PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTK	615
т79	541	TYPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIE	588
		.: ::   ::: :::::: :::: :::: ::::	
D45913			
T79		IEYVPRKSDAGISSADAPRKFNMKMI	
D45913	5 <b>66</b>	KKYMQKTSEIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY	714

FIG. 3B

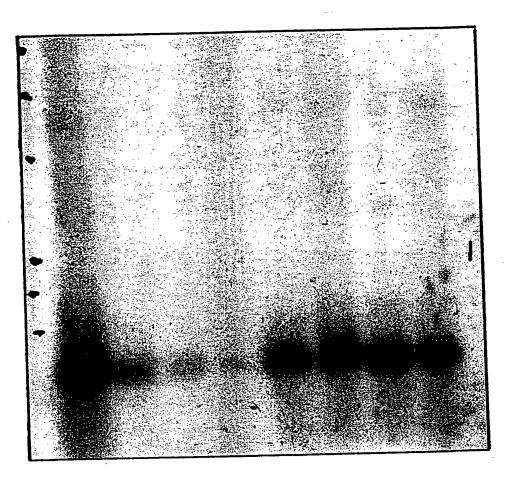


FIG. 4

Replacement Sheet

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A A L T L R N F C N W Q K Q H N P P S D  GOT GOO CITC ACT CITS COG AAC TITT TOO AAC TOG CAG AAG CAG CAC AAC CCC AGT GAC	39 119
R D A E H Y D T A I L F T R Q D L C G S COS GAT GOA GAS CAS GAS TOT TOT ACC AGA CAS GAS TOT TOT GOS TOT	59 179
Q T C D T L G M A D V G T V C D P S R S CAG ACA TOT GAT ACT CTT GGG ACC AGA ACT GTG TOT GAT CCG AGC AGA ACC	79 2 <b>39</b>
C S V I E D D G L Q A A F T T A H E L G TOC TOC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC CAT GAA TTA GGC	99 299 119
H V F N M P H D D A K Q C A S L N G V N CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG TGT GCC AGC CTT AAT GGT GTG AAC	359
Q D S H M M A S M L S N L D H S Q P W S CAG GAT TOO CAG ATG GOT TOO TOT TOO AAC CTT GAC CAC ACC CAG COT TOO TOT	4 <b>19</b> 159
COT TOO AGT GOO TAG ATG ATT ACA TOA TIT CITS GAT AAT GOT CAT GOO GAA TOT TITS ATG	179
GAC AAG COT CAG AAT COO ATA CAG CTO CCA GGC GAT CTO CO	539 . 199 599
AME COS CAS TOC CAS TIT ACA TIT COS GAS GAC TOC AAA CAS TOC CCI GAI GC. ST.	219
H F P W A D G T S C G E G K W C I N G K CAC TITC COC TOC GCC ACC TOT GCA GAA GCC AAA CAC TITC CCC TOC GCC GAT GGC ACC TOT GCA GAA GCC AAA TOC TOT ATC AAC GGC AAG	239
CAC THE COST TOS GOST GAT GOST ACT ACT TOT GOAR GAR GOST TOT GOST ACT TOS GOA ACC TOS GOA AAG CAT THE GAT ACG COT THE CAT GOA AGC TOS GOA ATC	259
W G P W G D C S R T C G G G V Q Y T M R TOG GGG GGT TGG GGA GAC TGT TGG AGA AGG TGC GGT GGA GGA GTC CAG TAC AGG ATG AG	279
E C D N P V P K N G G K Y C E G K R V R GAA TOT GAC AMC CCA GTC CCA AMG AMT GGA GGG AMG TAC TOT GAM GGC AMA CGA GTG CG	. 233
Y R S C N L E D C P D N N G R T F R E E TAC AGA TOC TOT AAC CTT GAG GAC TOT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GA	A 959
${\tt Q}$ C E A H N E F S K A S F G S G P A V ${\tt S}$ CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG CCT GGG GTG GG	A 1019
W I P K Y A G V S P K D R C K L I C Q X TOG ATT CCC AAG TAC GCT GGC GTC TCR CCA AAG GAC AGG TGC AAG CTC ATC TGC CAA G	
K G I G Y F F V L Q P K V V D G T P C  AMA GGC ATT GGC TAC TTC GTT TTG CAG CCC AAG GTT GTA GAT GGT ACT CCA TGT A	2 212

Docket/Appl'n No.: 10/718,332

Title: Novel Genes Encoding Proteins ... Inventors: Sean A. McCarthy, et al.

Replacement Sheet

S 7 C 7 Q G Q C 7 K A G C D CON GAT TOO ACC TOT GTG TOT GTG CAA GGA CAG TOT GTA AAA GCT GGT TOT GAT COC ACC 1199 V C G G N G S T C 419 K C G ATA GAC TOT ANA ANG ANG TITT GAT ANA TOT GGT GTT TOC GGG GGA ANT GGA TOT ACT TOT 1259 K K I S G S V T S A K P G Y H D I I ANA ANA ATA TOR GOA TOR GOT ROT ROT GOR ANA COT GOA THE CHE GHT ATC HOR ATT 1319 459 Q R G S R N 三 ソ K Q CCR ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT 1379 G S F L A I K A A D G T Y I L N G D Y T SEC ASC TIT CIT SEC ATC AAA SET SET GAT SEE ACA THE ATT CIT AAT SET GAE THE ACT 1439 R Y S G L V G M Y K THE TOO ACC THE GAS CAR GAD ATT AND THE AAR GOT GIT GITC THE AGE THE AGE GOD TOO 1499 E Q D I PLKEPLTI ALERIRS FS TOT GOG GOA TTG GAA AGA ATT CGC AGG TIT AGG CCT CTC AAA GAG CCC TTG ACC ATC CAG 1559 T Y F Y K K I K NALREE OTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG 1619 A W V I E E W G-T F s AMG AMG GAA TOT TTO AMT GOT ATO COO ACT TTT TOA GOA TOG GTC ATT GAA GAG TOG GGC 1679 Р K K R S LK K G Y GAN, TOT TOT AND ACC TOT GOO AND GOT THE ANA ANN AGA AGE THE AND TOT CTG TOE CAT 1739 E C S K T C G LKKPKHFI s c D Þ D G G V L S H E CAT COA COO GTG TTA TOT CAT GAG AGO TOT GAT COT TTA AAG AAA COT AAA CAT TTO ATA 1799 609 DFCTMAECS 1829 GAC TIT TOO ACA ATG GCA GAA TOO AGT TAA GIGGITTAAGIGGIGTTAGCTCTGAGGGCAAGGCCAAAGTGAGGAAGGGCTGGTGCAGGAAAGCCAGAAAGCTGGAGGG CATCAGAGTARACTOCCAGTTOCARATTTCATAGGATAGTTAGTGAGGATTATTAACCTCTGAGCAGTGATATAGCATA 2066 ATMANGECCESSGCATTATTATTATTATTTCTTTTGTTACATCTATTACAAGTTTAGRAAAAACAAAGCAATTGTCAAA 2145 AMAGTIAGRACTATTACAACCCCTGTTTCCTGGTACTTATCAAATACTTAGTATCATGGGTATGGAAATGAAAAGT 2224 ACCICALIMACITA CATATACA CONTENTA CONTENCIA ACANTOCCO CANACIA C CATTOTTC MACATER CRAMCOCT CAGCANCOT GAMATAACOCCARATOCCT TOCTOTTTTTTC GACCAT CTCA THECRITITALECCTOCTTTGGGATATATGGATGTAAGAAGTAACTTGTGTCTCATGAAAATCAGTACAATCACAAGG 2698

ACCATICADACCOCCURACAAAAATGACGTOTOTTACAACAGGTTCCCACAGGTTTCCGGACATTGACATCACTTGTCTTC	2777
TOTAL CONTROL OF THE PROPERTY	28 <b>56</b>
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ATTOGTTTOGGTGTTCCTTCCTAGAAGGACTATAGTTAGTTAGTAATAAATGCCTATAATAACATATTTATT	3014
ATTTCTAATGAAAAACTTTTAAATTATATCCCTTTTGTGGAAGTGCATATAAAATAGAGTATTTATACAATATATGT	
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FIG. 5C

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351 COTTLEMADVGTVCDPSRSCSVIEDD	CT OB A ETTERNET CHVENMPHIDAKH 400
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401 CASTAGUSGISHIMASMISSILIASC	PWSPCSAYMVISFILMENGECIADK 450
112 CASINGVNODSHMASALSILDIS	PWSPCSAYMITS*LINGBURIET 101
451 PONPIRLPSDLPGTLYCANROCQF	TEGETSKIEPDAASTCTTIMCTGTSG 500
162 PONPIQLEGDLEGTSYDANROCOFT	TGEDSKHEPDASICSTENCIGISC 211
501 GLLVCQTRHFFWADGTSCGBGRWC	VSGKCVNKTTEKHFATPVHGSWGFWG 550
212 GVLVCQTQHFPWADGTSCGEGKWC	:.
551 PWGDCSRTGGGGVQYTHREGENFV	PRINCERY COURT VRYRSCNIEDCEDN 600
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262 PWEDCSRICGGGVQYTHRECTHPV	PRINGERYCEGERVRYRSCNLEDCPDN 311
601 NIKTERFECCERHNEFSKASEGNE	PIVEWIPKYAGVSPKORCKLTCEARG 650
	1.[][.[][][][][][][][][][][][][][][][][]
312 NGKTFREEQCEAHNEFSKASFGSG	PAVENIPHYAGVSPKORCKLICCANG 361
	CVQCQCVKACCDRITESKKAFDKCGV 700
651 IGYFYUQPRVUGTPCSPDSIS	111111111111111111111111111111111111111
362 IGYFFVLQPKVVDGTPCSFDSTSV	CVQCQCVRAGERIIIISKKAFDKULV 411
701 CGCNGSTCKKNSGIVTSTRPGYH	DIVTIPAGATNIEVKHRNORGSRUNGS 750
412 CGCNGSTCKKISGSVTSAKPGYH	:   .      :
751 FLATRADGTYTLMENFTLSTLE	COLTYRGIVLRYSGSSAALERIRSFSP 800
1111:11(1111111::111111	DIMYKUVULKYSUSSAALERIRSFSP 511
801 IXEPLITIOVIMAHALREKIKET	YFMRKTESFNAIPITSEMVIFEMEEC 850
111111111 11:111111:1	11:111.1111111111111111
512 LEEPLTIQVLTVGNALRPKIKYT	YFVKKKESFNAIPITSAWVIEENGE. 560
901 WSPCSKTCGKGYKKRTLKCVSHI	GGVLSNESCOPLKEPRHYLDECTLIQC 950
[[[]]]]	:         :   :::  
951 s+ 951	THE VIDE CONTRACTOR THE COMMENT OF THE
1	FIG. 6
608 5* 609	110.0

gtgc	ctac	atg Met 1	gtc Val	acg Thr	tcc Ser	ttc Phe 5	cta Leu	gat Asp	aat Asn	gga Gly	cac His 10	Gly 999	gaa Glu	tg <b>t</b> Cys	t t g Leu	50
atg Met 15	gac Asp	aag Lys	ccc Pro	cag Gln	aat Asn 20	cca Pro	atc Ile	aag Lys	ctc Leu	ect Pro 25	tct Ser	gat Asp	ctt Leu	ccc Pro	ggt Gly 30	9 <b>8</b>
acc Thr	ttg Leu	tac Tyr	gat Asp	gcc Ala 35	aac Asn	cgc Arg	cag Gln	tg <b>t</b> Cys	cag Gln 40	ttt Phe	aca Thr	ttc Phe	gga Gly	gag Glu 45	gaa Glu	146
tcc Ser	aag Lys	cac His	tgc Cys 50	cct Pro	gat Asp	gca Ala	gcc Ala	agc Ser 55	aca Thr	tgt Cys	act Thr	acc Thr	ctg Leu 60	tgg Trp	tgc Cys	194
act Thr	ggc Gly	acc Thr 65	tc <b>c</b> Ser	ggt Gly	ggc Gly	tta Leu	ctg Leu 70	gtg Val	tgc Cys	caa Gln	aca Thr	aaa Lys 75	cac His	ttc Phe	cct Pro	242
tgg Trp	gca Ala 80	gat Asp	ggc Gly	acc Thr	agc Ser	tgt Cys 85	gga Gly	gaa Glu	gg <b>g</b> ggg	aag Lys	tgg Trp 90	tgt Cys	gtc Val	agt Ser	ggc	290
aag Lys 95	tgc Cys	gtg Val	aac Asn	aag Lys	aca Thr 100	gac Asp	atg .Met	aag Lys	cat His	ttt Phe 105	gct Ala	act Thr	cct Pro	gtt Val	cat His 110	338
gga Gly	agc Ser	tgg Trp	gga Gly	cca Pro 115	Trp	gga Gly	ccg Pro	tgg Trp	gga Gly 120	gac Asp	tgc Cys	tca Ser	aga Arg	acc Thr 125	tgt Cys	386
ggt Gly	ggt Gly	gga Gly	gtt Val 130	Gln	tac Tyr	aca Thr	atg Met	aga Arg 135	Glu	tgt Cys	gac A <b>sp</b>	aac Asn	cca Pro 140	Val	cca Pro	434
aag Lys	aac Asr	gga Gly 145	Gly	aag Lys	tac Tyr	tgt Cys	gaa Glu 150	Gly	aaa Lys	. cga : Arg	gtc Val	cgc Arg 155	tac Tyr	agg Arg	tcc Ser	482
tgt Cys	aac Asr 160	ı Ile	gaç Glu	g gad 1 Asi	c tgt o Cys	cca Pro	) Asp	aat Asi	aac 1 Asn	gga Gly	aaa Lys 170	Thr	ttc Phe	aga Arg	gag Glu	530
gag Glu 175	ı Glı	g tgo n Cys	gag Glu	g gcg	g cae a His	s Ası	gaq Glu	g ttt 1 Phe	tcc Ser	aaa Lys 185	Ala	tcc Ser	ttt Phe	ggg Gly	aat Asn 190	578
gaq Glu	g cce	c act	t gta	a gad 1 Gl 19	u Tr	g aca p Thi	a cco	c aaq o Ly:	g tac s Tyr 200	geo Ala	a Gly	y Val	. Sei	g cca Pro 205	) Lys	626

gac Asp	agg Arg	tgc Cys	aag Lys 210	ctc Leu	acc Thr	tg <b>t</b> Cys	gaa Glu	gcc Ala 215	aaa Lys	ggc Gly	att Ile	ggc	tac Tyr 220	ttt Phe	ttc Phe	674
gtc Val	tta Leu	cag Gln 225	cc <b>c</b> Pro	aag Lys	gtt Val	gta Val	gat Asp 230	ggc Gly	act Thr	ccc Pro	tgt Cys	agt Ser 235	cca Pro	gac Asp	tct Ser	722
acc Thr	tct Ser 240	gtc Val	tg <b>t</b> Cys	gtg Val	caa Gln	999 Gly 245	cag Gln	tgt Cys	gtg Val	aaa Lys	gct Ala 250	ggc	tgt Cys	gat Asp	cgc Arg	770
atc Ile 255	at <b>a</b> Ile	gac Asp	tcc Ser	aaa Lys	aag Lys 260	Lys	ttt Phe	gat Asp	aag Lys	tgt Cys 265	ggc Gly	gtt Val	tgt Cys	gga Gly	gga Gly 270	818
aac Asn	ggt	tco Sei	c aca	tgc Cys 275	: aag : Lys	aag Lys	atg Met	tca Ser	gga Gly 280	rie	gtc Val	act Thr	agt Ser	aca Thr 285	aga Arg	866
cct Pro	ggg Gly	g ta ⁄ Ty:	t cat r His	Ası	att o Ile	gto Val	aca Thr	att Ile 295	Pro	gct Ala	gga Gly	gcc Ala	acc Thr 300	aac Asn	att Ile	914
gaa	a gto ı Va	g aa l Ly 30	s Hi	t cgg	g aat g Asi	caa n Glr	a agg n Arg 310	g GIA	g tco / Sei	aga Arg	a aac g Asr	aat Asn 315	GIY	ago Ser	ttt phe	9 <b>62</b>
ct; Le	g gc u Al 32	a Il	t ag e Ar	a gc g Al	c gc a Al	t gat a Asi 32	b GT	t acc	c ta r Ty	t ati	t ctg e Lev 330	I ASI	gga Gly	aac Asr	ttC Phe	1010
Th 33	r Le 5	u Se	er Th	r Le	u Gl 34	u Gl O	n As	p Le	u Th	r 1y 34	т цу: 5	s GI	7 1111		tta Leu 350	1058
Ar	g Ty	r Se	er Gl	.y Se	er Se 55	r Al	a Al	a Le	u G1	u Ar	g II	e Ari	, se	36		1106
Pr	O Le	eu L	ys Gi	lu Pi 70	ro Le	eu Th	ır Il	.e G1 37	.n Va '5	ii re	u me	t va	38	0	t gct s Ala	
Le	eu A	rg P 3	ro L 85	ys I	le Ly	ys Pł	ne Th 39	ır Ty 90	r Pi	ie Me	ес гу	's цу	S гу	5 111	a gag r Glu	
t (	er P	tc a he A	ac g sn A	cc a la I	tt co le P	ro T	ca to hr Pl 05	ne Se	er G	ag to lu Ti	gg gt rp Va 41	11 11	e Gi	u Gi	g tgg	g 1250 p

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa   1346   Gln Cys Arg Aap Ile Aan Gly His Pro Ala Ser Glu Cys Ala Lys Glu   445    gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac   1394   Wal Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His   450    tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt   1442   Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly   465    tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta   1490   Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His   Asp Gly Gly Val Leu   485    tca aat gag agc tgt gat cct ttg aag ag cca aag cat tac att gac   1538   Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp   495    solon Solo Solo Solo Solo Solo Solo Solo	ggg gag tgc Gly Glu Cys 115	Ser Lys 1							1298
Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His  450  455  460  tgg cag gtg ggg gat tgg tca cca tgt tca aaa act tgc ggg aag ggt Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly  465  470  475  tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490  Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu  480  485  tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538  Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp 495  500  505  510  ttt tgc aca ctg ac ac gtgc agt taagaggggt tagagggacaa ggtagcgtgg 1592  Phe Cys Thr Leu Thr Gln Cys Ser  515  ggagggggtt atacactgag tgcaagagta ctggagggt caagtagagc gaacagta accactacact gcagttaca ttctgataag gaggattaatg aggacaagta ggactagag 1772  acactacaca agaatacaa ttctgaaag agcccaaaa cactattagt atctctttt ttatactat 1832  cgcccaaata attttcagag tgcgaagagaagaagaagagg agaagatgg aggacaaga aggacagaga aggacagaga aggacagaaga aggacagaga aggacaagaa ggcttgttta attcactaga gagacaagaa aggacagaga aggacaagaa caagataat attctgaaga gcttgttta aggagaaagaaga agaagagga agaagatggt tcaaacaaga 1952  gcttgtttc aatcactgag aggcaaagaaga gagaggacaaa caagatcatt attctgaaga gcttgtttc aatcactgag aggcaagaaga agaagatggt agaactaata ttcagaagt 2072  agcttgttca acgtgacaga aaggctcat tccgtgaaaga acaattcatc ttatactat 1832  cgcttgtttca acgtgacaga aaggctcat tccgtgaaaga acaattcatc tatacacag 1952  gcttgtttca acgtgacaga aaggctcat tccgtgaaaga acaattcatc tattataaa 2192  atgttacattg gaaaaaaaaa gtgaagttta tgaagtacaa ctagcattc tctttaca 2132  accatctcag ttcttaacta tagttcatgt tgaagataaa acaattcatc tatttaaaa 2192  atgttacattg gaaaaaaaaa gtgaagttta tgaagataaa acaattcatc tatttaaaa 2192  atggtgaatt tagagatca ggtcccatag agaagatga acaattcatc tatttataaa 2192  atggtgaatt tagagatca ggtccataga gagagacata atacaattat atttttaaa 2192  atggtgaatt tagagatca ctctactacag gagagaacat aatacaatta tatttttaaa 2292  tggtgaatt tatacaatat attgttaactta gaagagatat aatacaatt tatttttaaaa 2272  ctttattattc taatgataaa acctttaagt tatacctct ttgaaaaagt gactgtttc atagagatat 2372  ctttattatt		Asp Ile A			ro Ala			a Lys Glu	1346
Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly 465 470 475  tac aag aag aag aac ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu 480 485 480  tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp 495 500 505 510  ttt tgc aca ctg aca cag tgc agt taagaggggt tagaggacaa ggtagcgtgg 1592 Phe Cys Thr Leu Thr Gln Cys Ser 515  ggaggggctg atacactgag tgcaaggat ctggagggat ccagtgagtc aaaccagtaa 1652 gcagtgaggt gtggcaagga ggtgtgtg ggggatcat agcaacgag gtagatcagg 1712 acactaccct gccagttaca ttctgataag gcactattagt atctcttttc ttatactat 1832 cgcccaaata atttcagag tcgcaagaa gccccaaag cactattagt atctcttttc ttatactat 1832 cgcccaaata atttcagag tcgcaagaa gcactattagt atctcttttc ttatactat 1832 cgcccaaata atttcagag tctggcaagaa gccctattagt atctcttttc ttatactat 1832 cgttggttc atgagttaca tcggaggaga aggagacaaa caagatagt tcaaacaag 1952 gcttggtttc atcactgga ggcaaggagg aggaggacaaa caagatcatt attcgaagtc 2012 gctggttgct gtggtttac ggaaggttga tgcacaatc ctatcaacag tgaaacatt 2012 gctggttgct gtggttttac ggaaggttga tgcacatac ctatcacag tgaaaagtc 2012 gctggttgct gtggttttac ggaaggttga tgcacatac ctatcacag tgaaaagtc 2012 gctggttgct gtggttttac ggaaggttga tgcacatac ctatcacag tgaaaagtc 2012 gctggttgct gtggttttac ggaaggttga tgcacaaca caagatcatt attcgaagtc 2012 gctggttgct gtggtttac ggaaggttga tgcacaata ctatcacaag tgaaagatc 2012 gctggttgct gtggtttac ggaaggttga tgcacaaca caagatcatt tattcaaa 2192 accatccaa tactcacag aggaagtta tgcatcatc ctatcaacag tgaagaacaa 2252 tgagcaacat gctctcagct ttgcttcctc ctgaggtaaa ccagtcatt tatttaaa 2192 acgattacattg gaaaaaaaa ggaagtca ctcatcacag gagaagaaga caaagagaga aggagaacaa caaactcacac tattataaa ggaaggagct gtggaagag cacaagagag aggagaaa acaattcact tatttataaa ggaaggagct gctgaaggag tacacagagaga aggagaaaa acaattcact tatttataaa 2192 ggttgaatgt tatacataggt cacaagagag agaagaaaaa caattcact tatttataaa 2192 ggttgaatgt ctgttcagg cacaagagagagaa acaattaat tatttttata 2672 catttattct taatgataaa acctttaagt		Ala Ser		Pro C	ys Ala		u Pro Cy	s Pro His	1394
Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu 485 490  tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp 495 500 505 510  ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592 Phe Cys Thr Leu Thr Gln Cys Ser 515  ggaggggctg atacactgag tgcaagagta ctggagggat cagtagaggg gtagatcagg 1712 acactaccct gccagttaca ttctgataag ggggataat agcaagagag gtagatcagg 1712 acactaccct gccagttaca ttctggatag ggcccaaag cactatagt atctctttc tatatctat 1832 cgccaaata atttcagag tctggaaga ggccctatt acctatagt acctataga agcacagta aggcaagaga gggagacaa aggcaagaga gggggacaaa aggcacagta aggcatgagat ttctggcagaa gggggacaaa caagatcatt attcgaagtc 2012 gctggtttc aatcactgga ggcaagagag aggggacaaa caagatcatt attcgaagtc 2012 gctggtttc agtggtttac gggaaggagagagagagagagagagagagagagagag	Trp Gln Val	Gly Asp		Pro C	-		r Cys Gl		1442
Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp 500 505 510  ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592  Phe Cys Thr Leu Thr Gln Cys Ser 515  ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652 gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712 acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772 gaccatacag agcactaagg agcccaaag cactattagt atctctttt ttatatctat 1832 cgcccaaata attttcagag tctggcagaa ggccctgtc actgatacat ctagatactt 1892 cttatcacaa agattgggaa aggcaaagca gaaagatggt aagactgggt ttcaaacaag 1952 gcttggtttc aatcactgga ggcaaagagg aggggacaaa caagatcatt attcgaagtc 2012 gctggttgct gtggttttac ggaaggttga tgcatcatt ctatcaacag tgaaaggtc 2012 gcttggttgct gtggttttac ggaaggttga tgcatcatt ctatcaacag tgaaaggtc 2012 agcttgttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat tctttctac 2132 accatctcag ttcttaacta tagttcatgt tgaggtaaa acaattcatc tatttataaa 2192 atgacaacat gcctcctgct ttgcttcctc ctgaggagaa acaattcatc tatttataaa 2192 atgacaacat gcctcctgct ttgcttcctc ctgaggtaaa acaattcatc tatttataa 2292 atgaggaggt aagaatcag ggtcccatga gataaaataa tacatgttg gccaaggtt 2312 gcttaaggta tacacaggc aggagccaa ctcctggcag ctggtgatac ctcatccac 2432 atgggaggt ctgtcaaggt agaagstca ctcctggcag ctggtccaac agtgggaaca atggggaac atggtatcc 2492 tggtgaatgt ctgtcagct ctctactaa agtgaggaca ctctctggcag ctggtccaac agtgtatcc 2492 tggtgaatgt ctgtcagct ctctactaa agtgaggaca atggggaca tatttttata 2672 catttatttc taatgataaa acctttaagt tatacata atacatatt tattttata 2672 catttatttc taatgataaa acctttaagt tatactaa aagaacatt ttggagttgctgt 2792 atggcctattt tctggagtgg gattaactt tctggaagag ttgtatacta 2732 atagagtatt tctaacaatat atttttaga 2732 atagagtatt tctaacaatat atttttggg gattaactaa aagaacactt tttgaatgag 2792 atggcctattt tctggagtgg gattaacta attttcata 2672 catttattc taatgataaa acctttaagt tagagtacaa accaacacat ttatagacta 2792 atggcctattt tctggagtgg gattaacta attttcata 2672 aaatgactatt tctaaaaaa acctttaagt tagatgaaca ttattcctgt ttataagacg 2912 accaacacacacacacacacacacacacac	Tyr Lys Lys		Leu Lys			His As	p Gly Gl		1490
Phe Cys Thr Leu Thr Gln Cys Ser  515  ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652 gcagtgaggt gtggcaagga ggtgtgta ggggatacat agcaaaggag gtagatcagg 1712 acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcattgaaa 1772 gaccatacag agcactaagg agccccaaag cactattagt atctctttc ttatactat 1832 cgcccaaata attttcagag tctggcagaa gccctgttga actgtactaa ctagatactt 1892 cttatcacaa agattgggaa aggcaaagca gaaagatggt aagactgggt ttcaaacaag 1952 gcttggtttc aatcactga ggcaaggagg aggggacaaa cagatcatt attcgaagtc 2012 gctggttgct gtggtttac ggaaggttga tgcatcattc ctatcaacag tgaaagttc 2072 agcttgttca acgtgacaga aaggctcatc tccgtgaaag acaattcatt attctacac 2132 accatctcag ttcttaacta tagttcatgt tgaggtacaa acaattcatc tatttataaa 2192 atgtacattg gaaaaaaaaa gtgaagttta tgaggtacaa ataaaaacta aaggaacaac 2252 tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt 2312 gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta 2372 gaatggggta tagagatcag ggtcccatga ggtgggaac atggtgatca ctcatccac 2432 atgggaggtt gctgcagggt agcaggtcac ctcctggcag ctggtccaac agtcgtatc 2492 tggtgaatgt ctgttcagct cttcactga gagagatta gactgttcc atatgttcg gcagagtta 2552 gtatatagta aaatatgtta cttactagat catgactt tatacatgt ggttgtcttc 2612 tccttctaag aaggactata gctttaaata aatgcctata atacatgtt tttttata 2672 catttattc taatgataa acctttaagt tataccgtt ttgtaaaagt gcatataaaa 2732 atagagtatt tatacaatat atgtaacta gaataacta atacatgtt tttttata 2672 catttatttc taatgataa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732 atagagtatt tatacaatat atgttaactt tgggcaaga atcgatact ttgtaaagt 2792 atgcctattt tctggagtgg gattaacttc tgggcaaga atcgatct tttgtaaaac 2291 accatattaaaa aagaagttga tgatgtcttt agtggataaga ttttatcaa ttgtgggttgg 2912 actataaaaa aagaagttga tagtgtcttt agtggataaga ttttatcggt ttttcctgc 2912 actattagaaaaaaaaaaaaacaa ttttatgggt aaattagact ttttctctgc 3032	Ser Asn Glu	Ser Cys	Asp Pro			Pro Ly		r Ile Asp	1538
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	cgcccaaata cttatcacaa gcttggtttc gctggttgct agcttgttca accatctcag atgtacattg tgagcaacat gtttaagatt gaatggggta atgggaggct tggtgaatgt gtatatagta tccttctaag catttattc atagagtatt atgcctattt tggacttcaa actaataaaa	attttcaga agattggga aatcactgg gtggttta acgtgacag ttcttaact gaaaaaaa gcctcctgc atccatggc tagagatca gctgcaggg ctgttcagc aaatatgtt aaggactat taatgataa tatacaata tctggagtg gacagttt aagaagttt	g tetggga aggeagga aggeagga aagget agtgaagget tetget aggeagga agga	cagaa aagca ggtgg gttga catgt gtcatgt gtcatgt gtcatgt gtcatgt gtctt gatca gtctt gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatct gatca gatca gatct gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatca gatc	gccctgt gaaagat aggggac tgcgtga tgaggta tgaggta ctgaggta agtagag gagagaa catggcaa aatgcct gaaataa tgggcaa aatggcaa	tgc acressed	tgtactaa gactgggt agatcatt atcaacag tcctgat aaaaactgggt agtccaac tgtgtttcc aacaactt gatacattgt tttactgt tttactgt	ctagatacti ttcaaacaag attcgaagto tgaaaagto ttcttcttac tatttataaa aaggaaacaa gattgaggto gccagagtta ctcatctcac agtcgtatcc atatgtatata gtgtgtctgo tattttataaa ttgaatgtg tctaacaaaca ttatagacg	1892 1952 2012 2072 2132 2192 2252 2312 2372 2432 2432 2492 2552 2612 2672 2732 2792 2852 2912
gataaactgt ggctgtgctt taataaaact ttatttacaa aaaaaaaaaa	cgcccaaata cttatcacaa gcttggtttc gctggttgct agcttgttca accatctcag atgtacattg tgagcaacat gtttaagatt gaatggggta atgggaggct tggtgaatgt gtatatagta tccttctaag cattatttc atagagtatt atgcctattt tggacttcaa actaataaaa aaattgctgt	attttcaga agattggga aatcactgg gtggttta acgtgacag ttcttaact gaaaaaaa gcctcctgc atccatggc tagagatca gctgcaggg ctgttcagc aaatatgtt aaggactat taatgataa tctggagtg gacagttt aagaagttg aaagagcca	g tetggga aggeagga a aggeagga a taggtta agtteta agtteta aggeagga a	cagaa aagca ggtga ggtatga cattta gtcagga tcattta gtctgga aaacttc aacttc gtta aacttc gtta aacttc acttgt accttgt accttgt accttgt accttgt accttgt acctta accttc accttgt acctta accttc acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta a acctta a acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta acctta a acctta a acctta a a acctta a a a	gccctgt gaaagat aggggac tgcgtga tgaggta tgagggta ctgagggta gatgggaa catggca catgcctgg gagagaa catgtct gaaatgca taaataa tgggcaa aatggta ttatatgg	tgc acressed	tgtactaa gactgggt agatcacag ctcctgat aaaaactgggt cagtgttcaca ggtccaac ctgtattcg aacatagt gtacaacttg tacatagt tacatagt tacatagt tacatagt tacatagt tacatagt tacatagt	ctagatacti ttcaaacaag attcgaagto tgaaaagto ttcttcttac tatttataaa aaggaaacaa gattgaggto gccagagtta ctcatctcac agtcgtatcc atatgtatata gtgtgtctgo tatttttata ttgaatgtg acacaaaca ttatagacgo tgtggttgg	1892 1952 2012 2072 2132 2192 2252 2312 2372 2432 2492 2552 2612 2672 2732 2792 2852 2912 2972 3032

gegge cetga cegag cegag gegge	gago	ic co it go	egget eccta aggg	ecto agagt egego	ago gga gga	ccgci ccggi	get ( geg ( gea eag	ggee eeeg gagg agag gtg	aggg cccg tgtt agac agc	cg t gt a at g	ggga ggag ggag aggag	caga gaga tggt atg	c ag c cg g ac	acgg agga caag gca	acag gggg ccga ggg	180 240.
ggt a	atg a	aga Arg	agc Ser	atg Met 15	ccc ( Pro	agc c Ser P	cc c	tc d Leu I	Leu A	gcc t Ala (	cys (	rp (	ag d Sln 1	ecc a Pro I 25	itc [le	400
ctc (	ctg Leu	ctg Leu	gta Val 30	ctg Leu	gg <b>c</b> Gly	tca 9 Ser V	gtg o	Leu :	ser (	ggc 1	tct (	gct a Ala 1	Thr 40	ggc t Gly (	cya Cya	448
c <b>cg</b> Pro	ccc Pro	cgc Arg 45	tgc Cys	g <b>ag</b> Glu	tg <b>c</b> Cys	tca 9 Ser i	gcg ( Ala ( 50	cag Gln	gac Asp	cga ( Arg	gcc Ala	gtg Val 55	ctc Leu	tgc Cys	ca <b>c</b> His	496
cgc Arg	aaa Lys 60	cgc Arg	ttt Phe	gtg Val	gcg Ala	gtg Val 65	ccc Pro	gag Glu	ggc Gly	atc Ile	ece Pro 70	acc Thr	gag Glu	act Thr	cg <b>c</b> Arg	544
ctg Leu 75	ctg Leu	gac Asp	ctg Leu	ggc Gly	aaa Lys 80	aac Asn	cg <b>c</b> Arg	atc Ile	aag Lys	aca Thr 85	ctc Leu	a <b>a</b> c Asn	cag Gln	gac Asp	gag Glu 90	592
ttt Phe	gcc Ala	agc Ser	ttc Phe	cca Pro 95	His	ctg Leu	gag Glu	ga <b>g</b> Glu	cta Leu 100	gaa Glu	ctc Leu	aat Asn	gaa Glu	aac Asn 105	atc Ile	640
gtg Val	agc Ser	gcc	gtg Val	Glu	cca Pro	ggc Gly	gcc Ala	ttc Phe 115	aac Asn	aac Asn	ctc Leu	ttc Phe	aac Asn 120	ctg Leu	agg Arg	6 <b>88</b>
act Thr	ctg Leu	999 Gly 129	Le	g cgc	ago Ser	aac Asn	cgc Arg 130	ctg Leu	aag Lys	ctt Leu	atc Ile	ccg Pro 135	ctg Leu	ggc Gly	gtc Val	736
ttc Phe	acc Thi	Gl	c cto y Le	c ago u Sei	c aad	ttg Leu 145	acc Thr	aag Lys	ctg Leu	gac Asp	atc Ile 150	Ser	gag	aac 1 Asn	aag Lys	784
ato Ile 155	e Va	at l Il	c ct e Le	g cta u Lei	a gad u Asi 16	c tac p Tyr 0	atg Met	tto Phe	caa Glr	gac 1 Asp 165	Let	tac 1 Tyr	aac Ası	cto n Lev	aag 1 Lys 170	832
tcq Se:	g cte r Le	g ga u Gl	g gt u Va	c gg 1 G1 17	y As	c aac p Asn	gac Asp	c cto	gt: 1 Va: 180	и ГлАт	_ TT6	5 tcc Ser	. ni	t cga s Arg 18	y Ala	880

ttc Phe	agc Ser	ggc Gly	ctc Leu 190	aac Asn	agc Ser	ctg Leu	gaa Glu	cag Gln 195	ctg Leu	acg Thr	ctg Leu	gag Glu	aaa Lys 200	tgc Cys	aat Asn	928
ctg Leu	acc Thr	tcc Ser 205	atc Ile	ccc Pro	acg Thr	gag Glu	gcg Ala 210	ctc Leu	tcc Ser	cac His	ctg Leu	cac His 215	ggc Gly	ctc Leu	atc Ile	976
gtc Val	ctg Leu 220	cgg Arg	cta Leu	cga Arg	cat His	ctc Leu 225	aac Asn	atc Ile	aat Asn	gcc Ala	atc Ile 230	agg Arg	gac Asp	tac Tyr	tcc Ser	1024
ttc Phe 235	Lys	agg Arg	ctg Leu	tac Tyr	cga Arg 240	ctt Leu	aag Lys	gtc Val	tta Leu	gag Glu 245	atc Ile	tcc Ser	cac His	tgg Trp	ccc Pro 250	1072
tac Tyr	ctg Leu	gac Asp	acc Thr	ata Ile 255	Thr	ccc Pro	cgg Arg	acg Thr	cgt Arg 260	GJA aaa	tcg Ser		iG	8	R	1110

ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 6 ttgacagcca gtccgcccgt ccggagcccg gctcgttggg gcagc atg gcg ggg tcg 1 Met Ala Gly Ser 1																
							gcc Ala									.165
							ctg Leu									213
		_		-	_		agc Ser									261
	-				_	_	cgt Arg 60		_			_			2-2	309
							gcg Ala									357
			_	_			cgt Arg									405
							cag Gln									453
							gcc Ala								cca Pro	501
							ctg Leu 140									549
							cca Pro									597
							acc Thr				tga	ggta	ctt (	gctag	gggcgg	650
gtg	atceteaceg gaagttegga geeagagget geteetgeee egegeegeet eegeegatet gtggaeeagg atttgggtee egaggtgeee eetgagaaeg taetggggge tetgetaege gteaaaegee tggagaaeee etegeeeeag gegeeggeae geegeeteet geeteeetga													770		



Docket/Appl'n No.: 10/718,332

Title: Novel Genes Encoding Proteins ...

Inventors: Sean A. McCarthy, et al.
Replacement Sheet

FIG. 9B